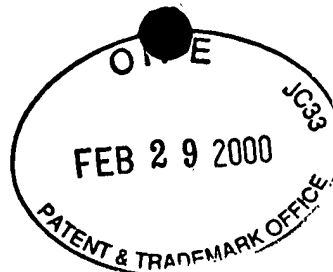


SEQUENCE LISTING



<110> Segre, Gino V.
Kronenberg, Henry M.
Abou-Samra, Abdul-Badi
Juppner, Harald
Potts, Jr., John T.
Schipani, Ernestina

<120> PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME

<130> 00786/071005

<140> US 09/199,874

<141> 1998-11-24

<150> US 08/471,494

<151> 1995-06-06

<160> 21

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1862

<212> DNA

<213> Didelphoidea

<220>

<221> CDS

<222> (98)...(1642)

<400> 1

tgggcacagc caccctgttg gtagtccagg ggccagccca ctgagctggc atatcagctg	60
gtggcccccgt tggactcggc cctaggggaac ggcggcg atg gga gcg ccc cgg atc	115
Met Gly Ala Pro Arg Ile	
1 5	
tcg cac agc ctt gcc ttg ctc ctc tgc tgc tcc gtg ctc agc tcc gtc	163
Ser His Ser Leu Ala Leu Leu Leu Cys Cys Ser Val Leu Ser Ser Val	
10 15 20	
tac gca ctg gtg gat gcc gat gat gtc ata acg aag gag gag cag atc	211
Tyr Ala Leu Val Asp Ala Asp Asp Val Ile Thr Lys Glu Glu Gln Ile	
25 30 35	
att ctt ctg cgc aat gcc cag gcc cag tgt gag cag cgc ctg aaa gag	259
Ile Leu Leu Arg Asn Ala Gln Ala Gln Cys Glu Gln Arg Leu Lys Glu	
40 45 50	
gtc ctc agg gtc cct gaa ctt gct gaa tct gcc aaa gac tgg atg tca	307
Val Leu Arg Val Pro Glu Leu Ala Glu Ser Ala Lys Asp Trp Met Ser	
55 60 65 70	
agg tct gca aag aca aag aag gag aaa cct gca gaa aag ctt tat ccc	355
Arg Ser Ala Lys Thr Lys Lys Glu Lys Pro Ala Glu Lys Leu Tyr Pro	
75 80 85	
cag gca gag gag tcc agg gaa gtt tct gac agg agc cgg ctg cag gat	403
Gln Ala Glu Glu Ser Arg Glu Val Ser Asp Arg Ser Arg Leu Gln Asp	
90 95 100	

ggc ttc tgc cta cct gag tgg gac aac att gtg tgc tgg cct gct gga Gly Phe Cys Leu Pro Glu Trp Asp Asn Ile Val Cys Trp Pro Ala Gly 105 110 115	451
gtg ccc ggc aag gtg gtg gcc gtg ccc tgc ccc gac tac ttc tac gac Val Pro Gly Lys Val Val Ala Val Pro Cys Pro Asp Tyr Phe Tyr Asp 120 125 130	499
ttc aac cac aaa ggc cga gcc tat cgg cgc tgt gac agc aat ggc agc Phe Asn His Lys Gly Arg Ala Tyr Arg Arg Cys Asp Ser Asn Gly Ser 135 140 145 150	547
tgg gag ctg gtg cct ggg aac aac cgg aca tgg gcg aat tac agc gaa Trp Glu Leu Val Pro Gly Asn Asn Arg Thr Trp Ala Asn Tyr Ser Glu 155 160 165	595
tgt gtc aag ttt ctg acc aac gag acc cgg gaa cgg gaa gtc ttt gat Cys Val Lys Phe Leu Thr Asn Glu Thr Arg Glu Arg Glu Val Phe Asp 170 175 180	643
cgc ctc gga atg atc tac act gtg ggc tac tcc atc tct ctg ggc tcc Arg Leu Gly Met Ile Tyr Thr Val Gly Tyr Ser Ile Ser Leu Gly Ser 185 190 195	691
ctc act gtg gct gtg ctg att ctg ggt tac ttt agg agg tta cat tgc Leu Thr Val Ala Val Leu Ile Leu Gly Tyr Phe Arg Arg Leu His Cys 200 205 210	739
acc cga aac tac att cac atg cat ctc ttc gtg tcc ttt atg ctc cgg Thr Arg Asn Tyr Ile His Met His Leu Phe Val Ser Phe Met Leu Arg 215 220 225 230	787
gct gta agc atc ttc atc aag gat gct gtg ctc tac tcg ggg gtt tcc Ala Val Ser Ile Phe Ile Lys Asp Ala Val Leu Tyr Ser Gly Val Ser 235 240 245	835
aca gat gaa atc gag cgc atc acc gag gag gag ctg agg gcc ttc aca Thr Asp Glu Ile Glu Arg Ile Thr Glu Glu Glu Leu Arg Ala Phe Thr 250 255 260	883
gag cct ccc cct gct gac aag gcg ggt ttt gtg ggc tgc aga gtg gcg Glu Pro Pro Pro Ala Asp Lys Ala Gly Phe Val Gly Cys Arg Val Ala 265 270 275	931
gta acc gtc ttc ctt tac ttc ctg acc acc aac tac tac tgg atc ctg Val Thr Val Phe Leu Tyr Phe Leu Thr Thr Asn Tyr Tyr Trp Ile Leu 280 285 290	979
gtg gaa ggc ctc tac ctt cac agc ctc atc ttc atg gct ttt ttc tct Val Glu Gly Leu Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser 295 300 305 310	1027
gag aaa aag tat ctc tgg ggt ttc aca tta ttt ggc tgg ggc ctc cct Glu Lys Lys Tyr Leu Trp Gly Phe Thr Leu Phe Gly Trp Gly Leu Pro 315 320 325	1075
gcc gtg ttt gtc gct gtg tgg gtg acc gtg agg gct aca ctg gcc aac Ala Val Phe Val Ala Val Trp Val Thr Val Arg Ala Thr Leu Ala Asn 330 335 340	1123

act gag tgc tgg gac ctg agt tgc ggg aat aag aaa tgg atc ata cag	1171
Thr Glu Cys Trp Asp Leu Ser Ser Gly Asn Lys Lys Trp Ile Ile Gln	
345 350 355	
gtg ccc atc ctg gca gct att gtg gtg aac ttt att ctt ttt atc aat	1219
Val Pro Ile Leu Ala Ala Ile Val Val Asn Phe Ile Leu Phe Ile Asn	
360 365 370	
ata atc aga gtc ctg gct act aaa ctc cgg gag acc aat gca ggg aga	1267
Ile Ile Arg Val Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg	
375 380 385 390	
tgt gac acg agg caa cag tat aga aag ctg ctg aag tcc acg cta gtc	1315
Cys Asp Thr Arg Gln Gln Tyr Arg Lys Leu Leu Lys Ser Thr Leu Val	
395 400 405	
ctc atg ccg cta ttt ggg gtg cac tac atc gtc ttc atg gcc acg ccg	1363
Leu Met Pro Leu Phe Gly Val His Tyr Ile Val Phe Met Ala Thr Pro	
410 415 420	
tac aca gaa gta tca ggg att ctt tgg caa gtc caa atg cac tat gaa	1411
Tyr Thr Glu Val Ser Gly Ile Leu Trp Gln Val Gln Met His Tyr Glu	
425 430 435	
atg ctc ttc aat tca ttc cag gga ttt ttc gtt gcc att ata tac tgt	1459
Met Leu Phe Asn Ser Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys	
440 445 450	
ttc tgc aat gga gag gta caa gca gag atc aag aag tca tgg agc cga	1507
Phe Cys Asn Gly Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg	
455 460 465 470	
tgg acc ctg gcc ttg gac ttc aag cgg aag gcc cgg agt ggc agc agt	1555
Trp Thr Leu Ala Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser	
475 480 485	
acc tac agc tat ggc ccc atg gtg tca cat aca agt gtc acc aat gtg	1603
Thr Tyr Ser Tyr Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val	
490 495 500	
gga cct cga ggg ggc tgg cct tgt ccc tca gcc ctc gac tagctcctgg	1652
Gly Pro Arg Gly Gly Trp Pro Cys Pro Ser Ala Leu Asp	
505 510 515	
ggctggagcc agtgccaatg gccatcacca gttgcctggc tatgtgaagc atggttccat	1712
ttctgagaac tcattgcctt catctggccc agagcctggc accaaagatg acgggtatct	1772
caatggctct ggactttatg agccaatggt tggggaacag cccctccac tcctggagga	1832
ggagagagag acagtcatgt gacccatata	1862

<210> 2

<211> 1863

<212> DNA

<213> Didelphoidea

<220>

<221> CDS

<222> (98)...(1852)

<400> 2

tgggacacag caccctgttg gtagtccagg ggccagccca ctgagctggc atatcagctg

60

gtggccccgt tggactcggc cctagggaac ggcggcg atg gga gcg ccc cgg atc	115
Met Gly Ala Pro Arg Ile	
1 5	
tcg cac agc ctt gcc ttg ctc ctc tgc tgc tcc gtg ctc agc tcc gtc	163
Ser His Ser Leu Ala Leu Leu Leu Cys Cys Ser Val Leu Ser Ser Val	
10 15 20	
tac gca ctg gtg gat gcc gat gat gtc ata acg aag gag gag cag atc	211
Tyr Ala Leu Val Asp Ala Asp Asp Val Ile Thr Lys Glu Glu Gln Ile	
25 30 35	
att ctt ctg cgc aat gcc cag gcc cag tgt gag cag cgc ctg aaa gag	259
Ile Leu Leu Arg Asn Ala Gln Ala Gln Cys Glu Gln Arg Leu Lys Glu	
40 45 50	
gtc ctc agg gtc cct gaa ctt gct gaa tct gcc aaa gac tgg atg tca	307
Val Leu Arg Val Pro Glu Leu Ala Glu Ser Ala Lys Asp Trp Met Ser	
55 60 65 70	
agg tct gca aag aca aag aag gag aaa cct gca gaa aag ctt tat ccc	355
Arg Ser Ala Lys Thr Lys Lys Glu Lys Pro Ala Glu Lys Leu Tyr Pro	
75 80 85	
cag gca gag gag tcc agg gaa gtt tct gac agg agc cgg ctg cag gat	403
Gln Ala Glu Glu Ser Arg Glu Val Ser Asp Arg Ser Arg Leu Gln Asp	
90 95 100	
ggc ttc tgc cta cct gag tgg gac aac att gtg tgc tgg cct gct gga	451
Gly Phe Cys Leu Pro Glu Trp Asp Asn Ile Val Cys Trp Pro Ala Gly	
105 110 115	
gtg ccc ggc aag gtg gtg gcc gtg ccc tgc ccc gac tac ttc tac gac	499
Val Pro Gly Lys Val Val Ala Val Pro Cys Pro Asp Tyr Phe Tyr Asp	
120 125 130	
ttc aac cac aaa ggc cga gcc tat cgg cgc tgt gac agc aat ggc agc	547
Phe Asn His Lys Gly Arg Ala Tyr Arg Arg Cys Asp Ser Asn Gly Ser	
135 140 145 150	
tgg gag ctg gtg cct ggg aac aac cgg aca tgg gcg aat tac agc gaa	595
Trp Glu Leu Val Pro Gly Asn Asn Arg Thr Trp Ala Asn Tyr Ser Glu	
155 160 165	
tgt gtc aag ttt ctg acc aac gag acc cgg gaa cgg gaa gtc ttt gat	643
Cys Val Lys Phe Leu Thr Asn Glu Thr Arg Glu Arg Glu Val Phe Asp	
170 175 180	
cgc ctc gga atg atc tac act gtg ggc tac tcc atc tct ctg ggc tcc	691
Arg Leu Gly Met Ile Tyr Thr Val Gly Tyr Ser Ile Ser Leu Gly Ser	
185 190 195	
ctc act gtg gct gtg ctg att ctg ggt tac ttt agg agg tta cat tgc	739
Leu Thr Val Ala Val Leu Ile Leu Gly Tyr Phe Arg Arg Leu His Cys	
200 205 210	
acc cga aac tac att cac atg cat ctc ttc gtg tcc ttt atg ctc cgg	787
Thr Arg Asn Tyr Ile His Met His Leu Phe Val Ser Phe Met Leu Arg	
215 220 225 230	

gct gta agc atc ttc atc aag gat gct gtg ctc tac tcg ggg gtt tcc Ala Val Ser Ile Phe Ile Lys Asp Ala Val Leu Tyr Ser Gly Val Ser 235 240 245	835
aca gat gaa atc gag cgc atc acc gag gag gag ctg agg gcc ttc aca Thr Asp Glu Ile Glu Arg Ile Thr Glu Glu Glu Leu Arg Ala Phe Thr 250 255 260	883
gag cct ccc cct gct gac aag gcg ggt ttt gtg ggc tgc aga gtg gcg Glu Pro Pro Pro Ala Asp Lys Ala Gly Phe Val Gly Cys Arg Val Ala 265 270 275	931
gta acc gtc ttc ctt tac ttc ctg acc acc aac tac tac tgg atc ctg Val Thr Val Phe Leu Tyr Phe Leu Thr Thr Asn Tyr Tyr Trp Ile Leu 280 285 290	979
gtg gaa ggc ctc tac ctt cac agc ctc atc ttc atg gct ttt ttc tct Val Glu Gly Leu Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser 295 300 305 310	1027
gag aaa aag tat ctc tgg ggt ttc aca tta ttt ggc tgg ggc ctc cct Glu Lys Lys Tyr Leu Trp Gly Phe Thr Leu Phe Gly Trp Gly Leu Pro 315 320 325	1075
gcc gtg ttt gtc gct gtg tgg gtg acc gtg agg gct aca ctg gcc aac Ala Val Phe Val Ala Val Trp Val Thr Val Arg Ala Thr Leu Ala Asn 330 335 340	1123
act gag tgc tgg gac ctg agt tcg ggg aat aag aaa tgg atc ata cag Thr Glu Cys Trp Asp Leu Ser Ser Gly Asn Lys Lys Trp Ile Ile Gln 345 350 355	1171
gtg ccc atc ctg gca gct att gtg gtg aac ttt att ctt ttt atc aat Val Pro Ile Leu Ala Ala Ile Val Val Asn Phe Ile Leu Phe Ile Asn 360 365 370	1219
ata atc aga gtc ctg gct act aaa ctc cgg gag acc aat gca ggg aga Ile Ile Arg Val Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg 375 380 385 390	1267
tgt gac acg agg caa cag tat aga aag ctg ctg aag tcc acg cta gtc Cys Asp Thr Arg Gln Gln Tyr Arg Lys Leu Leu Lys Ser Thr Leu Val 395 400 405	1315
ctc atg ccg cta ttt ggg gtg cac tac atc gtc ttc atg gcc acg ccg Leu Met Pro Leu Phe Gly Val His Tyr Ile Val Phe Met Ala Thr Pro 410 415 420	1363
tac aca gaa gta tca ggg att ctt tgg caa gtc caa atg cac tat gaa Tyr Thr Glu Val Ser Gly Ile Leu Trp Gln Val Gln Met His Tyr Glu 425 430 435	1411
atg ctc ttc aat tca ttc cag gga ttt ttc gtt gcc att ata tac tgt Met Leu Phe Asn Ser Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys 440 445 450	1459
ttc tgc aat gga gag gta caa gca gag atc aag aag tca tgg agc cga Phe Cys Asn Gly Glu Val Gln Ala Glu Ile Lys Lys Ser Trp S r Arg 455 460 465 470	1507

tgg acc ctg gcc ttg gac ttc aag cgg aag gcc cgg agt ggc agc agt	1555
Trp Thr Leu Ala Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser	
475 480 485	
acc tac agc tat ggc ccc atg gtg tca cat aca agt gtc acc aat gtg	1603
Thr Tyr Ser Tyr Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val	
490 495 500	
gga cct cga ggg ggg ctg gcc ttg tcc ctc agc cct cga cta gct cct	1651
Gly Pro Arg Gly Gly Leu Ala Leu Ser Leu Ser Pro Arg Leu Ala Pro	
505 510 515	
ggg gct gga gcc agt gcc aat ggc cat cac cag ttg cct ggc tat gtg	1699
Gly Ala Gly Ala Ser Ala Asn Gly His His Gln Leu Pro Gly Tyr Val	
520 525 530	
aag cat ggt tcc att tct gag aac tca ttg cct tca tct ggc cca gag	1747
Lys His Gly Ser Ile Ser Glu Asn Ser Leu Pro Ser Ser Gly Pro Glu	
535 540 545 550	
cct ggc acc aaa gat gac ggg tat ctc aat ggc tct gga ctt tat gag	1795
Pro Gly Thr Lys Asp Asp Gly Tyr Leu Asn Gly Ser Gly Leu Tyr Glu	
555 560 565	
cca atg gtt ggg gaa cag ccc cct cca ctc ctg gag gag gag aga gag	1843
Pro Met Val Gly Glu Gln Pro Pro Pro Leu Leu Glu Glu Glu Arg Glu	
570 575 580	
aca gtc atg tgacccatat c	1863
Thr Val Met	
585	

<210> 3
 <211> 2051
 <212> DNA
 <213> Rattus rattus

<220>
 <221> CDS
 <222> (73)...(1845)

<400> 3	
ggcggggggcc gcggcggcga gctcggaggc cggcggcggc tgccccgagg gacgcggccc	60
taggcggtgg cg atg ggg gcc gcc cgg atc gca ccc agc ctg gcg ctc cta	111
Met Gly Ala Ala Arg Ile Ala Pro Ser Leu Ala Leu Leu	
1 5 10	
ctc tgc tgc cca gtg ctc agc tcc gca tat gcg ctg gtg gat gcg gac	159
Leu Cys Cys Pro Val Leu Ser Ser Ala Tyr Ala Leu Val Asp Ala Asp	
15 20 25	
gat gtc ttt acc aaa gag gaa cag att ttc ctg ctg cac cgt gcc cag	207
Asp Val Phe Thr Lys Glu Glu Gln Ile Phe Leu Leu His Arg Ala Gln	
30 35 40 45	
gcg caa tgt gac aag ctg ctc aag gaa gtt ctg cac aca gca gcc aac	255
Ala Gln Cys Asp Lys Leu Leu Lys Glu Val Leu His Thr Ala Ala Asn	
50 55 60	

ata atg gag tca gac aag ggc tgg aca cca gca tct acg tca ggg aag Ile Met Glu Ser Asp Lys Gly Trp Thr Pro Ala Ser Thr Ser Gly Lys 65 70 75	303
ccc agg aaa gag aag gca tcg gga aag ttc tac cct gag tct aaa gag Pro Arg Lys Glu Lys Ala Ser Gly Lys Phe Tyr Pro Glu Ser Lys Glu 80 85 90	351
aac aag gac gtg ccc acc ggc agc agg cgc aga ggg cgt ccc tgt ctg Asn Lys Asp Val Pro Thr Gly Ser Arg Arg Arg Gly Arg Pro Cys Leu 95 100 105	399
ccc gag tgg gac aac atc gtt tgc tgg cca tta ggg gca cca ggt gaa Pro Glu Trp Asp Asn Ile Val Cys Trp Pro Leu Gly Ala Pro Gly Glu 110 115 120 125	447
gtg gtg gca gta cct tgt ccc gat tac att tat gac ttc aat cac aaa Val Val Ala Val Pro Cys Pro Asp Tyr Ile Tyr Asp Phe Asn His Lys 130 135 140	495
ggc cat gcc tac aga cgc tgt gac cgc aat ggc agc tgg gag gtg gtt Gly His Ala Tyr Arg Arg Cys Asp Arg Asn Gly Ser Trp Glu Val Val 145 150 155	543
cca ggg cac aac cgg acg tgg gcc aac tac agc gag tgc ctc aag ttc Pro Gly His Asn Arg Thr Trp Ala Asn Tyr Ser Glu Cys Leu Lys Phe 160 165 170	591
atg acc aat gag acg cgg gaa cgg gag gta ttt gac cgc cta ggc atg Met Thr Asn Glu Thr Arg Glu Arg Glu Val Phe Asp Arg Leu Gly Met 175 180 185	639
atc tac acc gtg gga tac tcc atg tct ctc gcc tcc ctc acg gtg gct Ile Tyr Thr Val Gly Tyr Ser Met Ser Leu Ala Ser Leu Thr Val Ala 190 195 200 205	687
gtg ctc atc ctg gcc tat ttt agg cgg ctg cac tgc acg cgc aac tac Val Leu Ile Leu Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn Tyr 210 215 220	735
atc cac atg cac atg ttc ctg tgc ttt atg ctg cgc gcc gcg agc atc Ile His Met His Met Phe Leu Ser Phe Met Leu Arg Ala Ala Ser Ile 225 230 235	783
ttc gtg aag gac gct gtg ctc tac tct ggc ttc acg ctg gat gag gcc Phe Val Lys Asp Ala Val Leu Tyr Ser Gly Phe Thr Leu Asp Glu Ala 240 245 250	831
gag cgc ctc aca gag gaa gag ttg cac atc atc gcg cag gtg cca cct Glu Arg Leu Thr Glu Glu Glu Leu His Ile Ile Ala Gln Val Pro Pro 255 260 265	879
ccg ccg gcc gct gcc gcc gta ggc tac gct ggc tgc cgc gtg gcg gtg Pro Pro Ala Ala Ala Val Gly Tyr Ala Gly Cys Arg Val Ala Val 270 275 280 285	927
acc ttc ttc ctc tac ttc ctg gct acc aac tac tac tgg att ctg gtg Thr Phe Phe Leu Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val 290 295 300	975

gag ggg ctg tac ttg cac agc ctc atc ttc atg gcc ttt ttc tca gag Glu Gly Leu Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser Glu 305 310 315	1023
aag aag tac ctg tgg ggc ttc acc atc ttt ggc tgg ggt cta ccg gct Lys Lys Tyr Leu Trp Gly Phe Thr Ile Phe Gly Trp Gly Leu Pro Ala 320 325 330	1071
gtc ttc gtg gct gtg tgg gtc ggt gtc aga gca acc ttg gcc aac act Val Phe Val Ala Val Trp Val Gly Val Arg Ala Thr Leu Ala Asn Thr 335 340 345	1119
ggg tgc tgg gat ctg agc tcc ggg cac aag aag tgg atc atc cag gtg Gly Cys Trp Asp Leu Ser Ser Gly His Lys Lys Trp Ile Ile Gln Val 350 355 360 365	1167
ccc atc ctg gca tct gtt gtg ctc aac ttc atc ctt ttt atc aac atc Pro Ile Leu Ala Ser Val Val Leu Asn Phe Ile Leu Phe Ile Asn Ile 370 375 380	1215
atc cgg gtg ctt gcc act aag ctt cgg gag acc aat gcg ggc cgg tgt Ile Arg Val Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys 385 390 395	1263
gac acc agg cag cag tac cgg aag ctg ctc agg tcc acg ttg gtg ctc Asp Thr Arg Gln Gln Tyr Arg Lys Leu Leu Arg Ser Thr Leu Val Leu 400 405 410	1311
gtg ccg ctc ttt ggt gtc cac tac acc gtc ttc atg gcc ttg ccg tac Val Pro Leu Phe Gly Val His Tyr Thr Val Phe Met Ala Leu Pro Tyr 415 420 425	1359
acc gag gtc tca ggg aca ttg tgg cag atc cag atg cat tat gag atg Thr Glu Val Ser Gly Thr Leu Trp Gln Ile Gln Met His Tyr Glu Met 430 435 440 445	1407
ctc ttc aac tcc ttc cag gga ttt ttt gtt gcc atc ata tac tgt ttc Leu Phe Asn Ser Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe 450 455 460	1455
tgc aat ggt gag gtg cag gca gag att agg aag tca tgg agc cgc tgg Cys Asn Gly Glu Val Gln Ala Glu Ile Arg Lys Ser Trp Ser Arg Trp 465 470 475	1503
aca ctg gcg ttg gac ttc aag cgc aaa gca cga agt ggg agt agc agc Thr Leu Ala Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser 480 485 490	1551
tac agc tat ggc cca atg gtg tct cac acg agt gtg acc aat gtg ggc Tyr Ser Tyr Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly 495 500 505	1599
ccc cgt gca gga ctc agc ctc ccc ctc agc ccc cgc ctg cct cct gcc Pro Arg Ala Gly Leu Ser Leu Pro Leu Ser Pro Arg Leu Pro Pro Ala 510 515 520 525	1647
act acc aat ggc cac tcc cag ctg cct ggc cat gcc aag cca ggg gct Thr Thr Asn Gly His Ser Gln Leu Pro Gly His Ala Lys Pro Gly Ala 530 535 540	1695

cca gcc act gag act gaa acc cta cca gtc act atg gcg gtt ccc aag 1743
 Pro Ala Thr Glu Thr Glu Thr Leu Pro Val Thr Met Ala Val Pro Lys
 545 550 555

gac gat gga ttc ctt aac ggc tcc tgc tca ggc ctg gat gag gag gcc 1791
 Asp Asp Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala
 560 565 570

tcc ggg tct gcg cgg ccg cct cca ttg ttg cag gaa gga tgg gaa aca 1839
 Ser Gly Ser Ala Arg Pro Pro Leu Leu Gln Glu Gly Trp Glu Thr
 575 580 585

gtc atg tgactgggca ctagggggct agactgctgg cctgggcaca tggacagatg 1895
 Val Met
 590

gaccaagaag ccagtgtttg gctggttgct tattcgggat ctggaccagg aagataacaa 1955
 aaggaaaatg gaagtggacg aagcagagaa gaaggaagag gttttgcagg aattaaatat 2015
 gtttcctcag ttggatgatg aggacacaag gaaggc 2051

<210> 4
 <211> 2010
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (28)...(1806)

<400> 4
 gggatccccgc ggccctaggc ggtggcg atg ggg acc gcc cgg atc gca ccc ggc 54
 Met Gly Thr Ala Arg Ile Ala Pro Gly
 1 5

ctg gcg ctc ctg ctc tgc tgc ccc gtg ctc agc tcc gcg tac gcg ctg 102
 Leu Ala Leu Leu Leu Cys Cys Pro Val Leu Ser Ser Ala Tyr Ala Leu
 10 15 20 25

gtg gat gca gat gac gtc atg act aaa gag gaa cag atc ttc ctg ctg 150
 Val Asp Ala Asp Asp Val Met Thr Lys Glu Glu Gln Ile Phe Leu Leu
 30 35 40

cac cgt gct cag gcc cag tgc gaa aaa cgg ctc aag gag gtc ctg cag 198
 His Arg Ala Gln Ala Gln Cys Glu Lys Arg Leu Lys Glu Val Leu Gln
 45 50 55

agg cca gcc agc ata atg gaa tca gac aag gga tgg aca tct gcg tcc 246
 Arg Pro Ala Ser Ile Met Glu Ser Asp Lys Gly Trp Thr Ser Ala Ser
 60 65 70

aca tca ggg aag ccc agg aaa gat aag gca tct ggg aag ctc tac cct 294
 Thr Ser Gly Lys Pro Arg Lys Asp Lys Ala Ser Gly Lys Leu Tyr Pro
 75 80 85

gag tct gag gag gac aag gag gca ccc act ggc agc agg tac cga ggg 342
 Glu Ser Glu Glu Asp Lys Glu Ala Pro Thr Gly Ser Arg Tyr Arg Gly
 90 95 100 105

cgc ccc tgt ctg ccg gaa tgg gac cac atc ctg tgc tgg ccg ctg ggg 390
 Arg Pro Cys Leu Pro Glu Trp Asp His Ile Leu Cys Trp Pro Leu Gly
 110 115 120

gca cca ggt gag gtg gtg gct gtg ccc tgt ccg gac tac att tat gac Ala Pro Gly Glu Val Val Ala Val Pro Cys Pro Asp Tyr Ile Tyr Asp 125 130 135	438
ttc aat cac aaa ggc cat gcc tac cga cgc tgt gac cgc aat ggc agc Phe Asn His Lys Gly His Ala Tyr Arg Arg Cys Asp Arg Asn Gly Ser 140 145 150	486
tgg gag ctg gtg cct ggg cac aac agg acg tgg gcc aac tac agc gag Trp Glu Leu Val Pro Gly His Asn Arg Thr Trp Ala Asn Tyr Ser Glu 155 160 165	534
tgt gtc aaa ttt ctc acc aat gag act cgt gaa cgg gag gtg ttt gac Cys Val Lys Phe Leu Thr Asn Glu Thr Arg Glu Arg Glu Val Phe Asp 170 175 180 185	582
cgc ctg ggc atg att tac acc gtg ggc tac tcc gtg tcc ctg gcg tcc Arg Leu Gly Met Ile Tyr Thr Val Gly Tyr Ser Val Ser Leu Ala Ser 190 195 200	630
ctc acc gta gct gtg ctc atc ctg gcc tac ttt agg cgg ctg cac tgc Leu Thr Val Ala Val Leu Ile Leu Ala Tyr Phe Arg Arg Leu His Cys 205 210 215	678
acg cgc aac tac atc cac atg cac ctg ttc ctg tcc ttc atg ctg cgc Thr Arg Asn Tyr Ile His Met His Leu Phe Leu Ser Phe Met Leu Arg 220 225 230	726
gcc gtg agc atc ttc gtc aag gac gct gtg ctc tac tct ggc gcc acg Ala Val Ser Ile Phe Val Lys Asp Ala Val Leu Tyr Ser Gly Ala Thr 235 240 245	774
ctt gat gag gct gag cgc ctc acc gag gag gag ctg cgc gcc atc gcc Leu Asp Glu Ala Glu Arg Leu Thr Glu Glu Glu Leu Arg Ala Ile Ala 250 255 260 265	822
cag gcg ccc ccg ccg cct gcc acc gcc gct gcc ggc tac gcg ggc tgc Gln Ala Pro Pro Pro Ala Thr Ala Ala Ala Gly Tyr Ala Gly Cys 270 275 280	870
agg gtg gct gtg acc ttc ttc ctt tac ttc ctg gcc acc aac tac tac Arg Val Ala Val Thr Phe Phe Leu Tyr Phe Leu Ala Thr Asn Tyr Tyr 285 290 295	918
tgg att ctg gtg gag ggg ctg tac ctg cac agc ctc atc ttc atg gcc Trp Ile Leu Val Glu Gly Leu Tyr Leu His Ser Leu Ile Phe Met Ala 300 305 310	966
ttc ttc tca gag aag aag tac ctg tgg ggc ttc aca gtc ttc ggc tgg Phe Phe Ser Glu Lys Lys Tyr Leu Trp Gly Phe Thr Val Phe Gly Trp 315 320 325	1014
ggc ctg ccc gct gtc ttc gtg gct gtg tgg gtc agt gtc aga gct acc Gly Leu Pro Ala Val Phe Val Ala Val Trp Val Ser Val Arg Ala Thr 330 335 340 345	1062
ctg gcc aac acc ggg tgc tgg gac ttg agc tcc ggg aac aaa aag tgg Leu Ala Asn Thr Gly Cys Trp Asp Leu Ser Ser Gly Asn Lys Lys Trp 350 355 360	1110

atc atc cag gtg ccc atc ctg gcc tcc att gtg ctc aac ttc atc ctc Ile Ile Gln Val Pro Ile Leu Ala Ser Ile Val Leu Asn Phe Ile Leu 365 370 375	1158
ttc atc aat atc gtc cgg gtg ctc gcc acc aag cag cgg gag acc aac Phe Ile Asn Ile Val Arg Val Leu Ala Thr Lys Gln Arg Glu Thr Asn 380 385 390	1206
gcc ggc cgg tgt gac aca cgg cag cag tac cgg aag ctg ctc aaa tcc Ala Gly Arg Cys Asp Thr Arg Gln Gln Tyr Arg Lys Leu Leu Lys Ser 395 400 405	1254
acg ctg gtg ctc atg ccc ctc ttt ggc gtc cac tac att gtc ttc atg Thr Leu Val Leu Met Pro Leu Phe Gly Val His Tyr Ile Val Phe Met 410 415 420 425	1302
gcc aca cca tac acc gag gtc tca ggg acg ctc tgg caa gtc cag atg Ala Thr Pro Tyr Thr Glu Val Ser Gly Thr Leu Trp Gln Val Gln Met 430 435 440	1350
cac tat gag atg ctc ttc aac tcc ttc cag gga ttt ttt gtc gca atc His Tyr Glu Met Leu Phe Asn Ser Phe Gln Gly Phe Phe Val Ala Ile 445 450 455	1398
ata tac tgt ttc tgc aat ggc gag gta caa gct gag atc aag aaa tct Ile Tyr Cys Phe Cys Asn Gly Glu Val Gln Ala Glu Ile Lys Lys Ser 460 465 470	1446
tgg agc cgc tgg aca ctg gca ctg gac ttc aag cga aag gca cgc agc Trp Ser Arg Trp Thr Leu Ala Leu Asp Phe Lys Arg Lys Ala Arg Ser 475 480 485	1494
ggg agc agc agc tat agc tac ggc ccc atg gtg tcc cac aca agt gtg Gly Ser Ser Ser Tyr Ser Tyr Gly Pro Met Val Ser His Thr Ser Val 490 495 500 505	1542
acc aat gtc ggc ccc cgt gtg gga ctc ggc ctg ccc ctc agc ccc cgc Thr Asn Val Gly Pro Arg Val Gly Leu Gly Leu Pro Leu Ser Pro Arg 510 515 520	1590
cta ctg ccc act gcc acc acc aac ggc cac cct cag ctg cct ggc cat Leu Leu Pro Thr Ala Thr Thr Asn Gly His Pro Gln Leu Pro Gly His 525 530 535	1638
gcc aag cca ggg acc cca gcc ctg gag acc ctc gag acc aca cca cct Ala Lys Pro Gly Thr Pro Ala Leu Glu Thr Leu Glu Thr Thr Pro Pro 540 545 550	1686
gcc atg gct gct ccc aag gac gat ggg ttc ctc aac ggc tcc tgc tca Ala Met Ala Ala Pro Lys Asp Asp Gly Phe Leu Asn Gly Ser Cys Ser 555 560 565	1734
ggc ctg gac gag gag gcc tct ggg cct gag cgg cca cct gcc ctg cta Gly Leu Asp Glu Glu Ala Ser Gly Pro Glu Arg Pro Pro Ala Leu Leu 570 575 580 585	1782
cag gaa gag tgg gag aca gtc atg tgaccaggcg ctgggggctg gacctgctga Gln Glu Glu Trp Glu Thr Val Met 590	1836
catagtggat ggacagatgg accaaaagat ggggtggttga atgattttccc actcaggggcc tggggccaag agggaaaaaac aggggaaaaaa agaaaaaaa aagaaaaaag gaaaaaaa	1896 1956

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa

2010

```
<210> 5
<211> 20
<212> PRT
<213> Artificial Sequence
```

```
<220>
<223> binding; 1st to last; peptide fragment
```

```

<400> 5
Thr Asn Glu Thr Arg Glu Arg Glu Val Phe Asp Arg Leu Gly Met Ile
  1           5           10           15
Tyr Thr Val Gly
           20

```

```
<210> 6
<211> 19
<212> PRT
<213> Artificial Sequence
```

<220>
<223> binding; 1st to last; peptide fragment

<400> 6
Tyr Leu Tyr Ser Gly Phe Thr Leu Asp Glu Ala Glu Arg Leu Thr Glu
1 5 10 15
Glu Glu Leu

```
<210> 7
<211> 19
<212> PRT
<213> Artificial Sequence
```

```
<220>
<223> binding; 1st to last; peptide fragment
```

```

<400> 7
Val Thr Phe Phe Leu Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu
  1             5             10             15
Val Glu Gly

```

```
<210> 8
<211> 26
<212> PRT
<213> Artificial Sequence
```

<220>
<223> binding; 1st to last; peptide fragment

```
<221> VARIANT
<222> (1)...(26)
<223> Xaa = Any Amino Acid
```

```

<400> 8
Tyr Xaa Arg Ala Thr Leu Ala Asn Thr Gly Cys Trp Asp Leu Ser Ser
  1          5          10          15
Gly His Lys Lys Trp Ile Ile Gln Val Pro
      20          25

```

<210> 9
 <211> 18
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> binding; 1st to last; peptide fragment

<400> 9
 Pro Tyr Thr Glu Tyr Ser Gly Thr Leu Trp Gln Ile Gln Met His Tyr
 1 5 10 15
 Glu Met

<210> 10
 <211> 18
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> binding; 1st to last; peptide fragment

<400> 10
 Asp Asp Val Phe Thr Lys Glu Glu Gln Ile Phe Leu Leu His Arg Ala
 1 5 10 15
 Gln Ala

<210> 11
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> binding; 1st to last; peptide fragment

<400> 11
 Phe Phe Arg Leu His Cys Thr Arg Asn Tyr
 1 5 10

<210> 12
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> binding; 1st to last; peptide fragment

<400> 12
 Glu Lys Lys Tyr Leu Trp Gly Phe Thr Leu
 1 5 10

<210> 13
 <211> 25
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> binding; 1st to last; peptide fragment

<400> 13
 Val L u Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr
 1 5 10 15
 Arg Gln Gln Tyr Arg Lys Leu Leu Lys
 20 25

<210> 14
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 1st to last; primer

<400> 14
 agatgaggct gtgcaggt

18

<210> 15
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 1st to last; primer

<400> 15
 ggaattccat gggagcggcc cggat

25

<210> 16
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 1st to last; primer

<400> 16
 cgggatcccg cggccctagg cggat

24

<210> 17
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 1st to last; primer

<400> 17
 agtatagcgt ccttgacga

19

<210> 18
 <211> 515
 <212> PRT
 <213> Didelphoidea

<400> 18
 Met Gly Ala Pro Arg Ile Ser His Ser Leu Ala Leu Leu Cys Cys
 1 5 10 15
 Ser Val Leu Ser Ser Val Tyr Ala Leu Val Asp Ala Asp Asp Val Ile
 20 25 30
 Thr Lys Glu Glu Ile Ile Leu Arg Asn Ala Gln Ala Gln Cys
 35 40 45

Glu	Gln	Arg	Leu	Lys	Glu	Val	Leu	Arg	Val	Pro	Glu	Leu	Ala	Glu	Ser
50					55					60					
Ala	Lys	Asp	Trp	Met	Ser	Arg	Ser	Ala	Lys	Thr	Lys	Lys	Glu	Lys	Pro
65					70					75					80
Ala	Glu	Lys	Leu	Tyr	Pro	Gln	Ala	Glu	Glu	Ser	Arg	Glu	Val	Ser	Asp
				85					90					95	
Arg	Ser	Arg	Leu	Gln	Asp	Gly	Phe	Cys	Leu	Pro	Glu	Trp	Asp	Asn	Ile
			100				105						110		
Val	Cys	Trp	Pro	Ala	Gly	Val	Pro	Gly	Lys	Val	Val	Ala	Val	Pro	Cys
		115				120						125			
Pro	Asp	Tyr	Phe	Tyr	Asp	Phe	Asn	His	Lys	Gly	Arg	Ala	Tyr	Arg	Arg
		130				135					140				
Cys	Asp	Ser	Asn	Gly	Ser	Trp	Glu	Leu	Val	Pro	Gly	Asn	Asn	Arg	Thr
145					150					155					160
Trp	Ala	Asn	Tyr	Ser	Glu	Cys	Val	Lys	Phe	Leu	Thr	Asn	Glu	Thr	Arg
				165					170					175	
Glu	Arg	Glu	Val	Phe	Asp	Arg	Leu	Gly	Met	Ile	Tyr	Thr	Val	Gly	Tyr
			180					185					190		
Ser	Ile	Ser	Leu	Gly	Ser	Leu	Thr	Val	Ala	Val	Leu	Ile	Leu	Gly	Tyr
		195					200					205			
Phe	Arg	Arg	Leu	His	Cys	Thr	Arg	Asn	Tyr	Ile	His	Met	His	Leu	Phe
		210				215					220				
Val	Ser	Phe	Met	Leu	Arg	Ala	Val	Ser	Ile	Phe	Ile	Lys	Asp	Ala	Val
225					230					235					240
Leu	Tyr	Ser	Gly	Val	Ser	Thr	Asp	Glu	Ile	Glu	Arg	Ile	Thr	Glu	Glu
				245					250					255	
Glu	Leu	Arg	Ala	Phe	Thr	Glu	Pro	Pro	Pro	Ala	Asp	Lys	Ala	Gly	Phe
			260					265					270		
Val	Gly	Cys	Arg	Val	Ala	Val	Thr	Val	Phe	Leu	Tyr	Phe	Leu	Thr	Thr
		275					280					285			
Asn	Tyr	Tyr	Trp	Ile	Leu	Val	Glu	Gly	Leu	Tyr	Leu	His	Ser	Leu	Ile
		290				295					300				
Phe	Met	Ala	Phe	Phe	Ser	Glu	Lys	Lys	Tyr	Leu	Trp	Gly	Phe	Thr	Leu
305					310					315					320
Phe	Gly	Trp	Gly	Leu	Pro	Ala	Val	Phe	Val	Ala	Val	Trp	Val	Thr	Val
				325					330					335	
Arg	Ala	Thr	Leu	Ala	Asn	Thr	Glu	Cys	Trp	Asp	Leu	Ser	Ser	Gly	Asn
			340					345					350		
Lys	Lys	Trp	Ile	Ile	Gln	Val	Pro	Ile	Leu	Ala	Ala	Ile	Val	Val	Asn
		355					360					365			
Phe	Ile	Leu	Phe	Ile	Asn	Ile	Ile	Arg	Val	Leu	Ala	Thr	Lys	Leu	Arg
		370				375					380				
Glu	Thr	Asn	Ala	Gly	Arg	Cys	Asp	Thr	Arg	Gln	Gln	Tyr	Arg	Lys	Leu
385					390					395					400
Leu	Lys	Ser	Thr												

<210> 19
 <211> 585
 <212> PRT
 <213> Didelphoid a

<400> 19
 Met Gly Ala Pro Arg Ile Ser His Ser Leu Ala Leu Leu Leu Cys Cys
 1 5 10 15
 Ser Val Leu Ser Ser Val Tyr Ala Leu Val Asp Ala Asp Asp Val Ile
 20 25 30
 Thr Lys Glu Glu Gln Ile Ile Leu Leu Arg Asn Ala Gln Ala Gln Cys
 35 40 45
 Glu Gln Arg Leu Lys Glu Val Leu Arg Val Pro Glu Leu Ala Glu Ser
 50 55 60
 Ala Lys Asp Trp Met Ser Arg Ser Ala Lys Thr Lys Lys Glu Lys Pro
 65 70 75 80
 Ala Glu Lys Leu Tyr Pro Gln Ala Glu Glu Ser Arg Glu Val Ser Asp
 85 90 95
 Arg Ser Arg Leu Gln Asp Gly Phe Cys Leu Pro Glu Trp Asp Asn Ile
 100 105 110
 Val Cys Trp Pro Ala Gly Val Pro Gly Lys Val Val Ala Val Pro Cys
 115 120 125
 Pro Asp Tyr Phe Tyr Asp Phe Asn His Lys Gly Arg Ala Tyr Arg Arg
 130 135 140
 Cys Asp Ser Asn Gly Ser Trp Glu Leu Val Pro Gly Asn Asn Arg Thr
 145 150 155 160
 Trp Ala Asn Tyr Ser Glu Cys Val Lys Phe Leu Thr Asn Glu Thr Arg
 165 170 175
 Glu Arg Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr Val Gly Tyr
 180 185 190
 Ser Ile Ser Leu Gly Ser Leu Thr Val Ala Val Leu Ile Leu Gly Tyr
 195 200 205
 Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met His Leu Phe
 210 215 220
 Val Ser Phe Met Leu Arg Ala Val Ser Ile Phe Ile Lys Asp Ala Val
 225 230 235 240
 Leu Tyr Ser Gly Val Ser Thr Asp Glu Ile Glu Arg Ile Thr Glu Glu
 245 250 255
 Glu Leu Arg Ala Phe Thr Glu Pro Pro Ala Asp Lys Ala Gly Phe
 260 265 270
 Val Gly Cys Arg Val Ala Val Thr Val Phe Leu Tyr Phe Leu Thr Thr
 275 280 285
 Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu Tyr Leu His Ser Leu Ile
 290 295 300
 Phe Met Ala Phe Phe Ser Glu Lys Lys Tyr Leu Trp Gly Phe Thr Leu
 305 310 315 320
 Phe Gly Trp Gly Leu Pro Ala Val Phe Val Ala Val Trp Val Thr Val
 325 330 335
 Arg Ala Thr Leu Ala Asn Thr Glu Cys Trp Asp Leu Ser Ser Gly Asn
 340 345 350
 Lys Lys Trp Ile Ile Gln Val Pro Ile Leu Ala Ala Ile Val Val Asn
 355 360 365
 Phe Ile Leu Phe Ile Asn Ile Ile Arg Val Leu Ala Thr Lys Leu Arg
 370 375 380
 Glu Thr Asn Ala Gly Arg Cys Asp Thr Arg Gln Gln Tyr Arg Lys Leu
 385 390 395 400
 Leu Lys Ser Thr Leu Val Leu Met Pro Leu Phe Gly Val His Tyr Ile
 405 410 415
 Val Phe Met Ala Thr Pro Tyr Thr Glu Val Ser Gly Ile Leu Trp Gln
 420 425 430
 Val Gln Met His Tyr Glu Met Leu Phe Asn Ser Phe Gln Gly Phe Phe
 435 440 445

Val Ala Ile Ile Tyr Cys Phe Cys Asn Gly Glu Val Gln Ala Glu Ile
 450 455 460
 Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala Leu Asp Phe Lys Arg Lys
 465 470 475 480
 Ala Arg Ser Gly Ser Ser Thr Tyr Ser Tyr Gly Pro Met Val Ser His
 485 490 495
 Thr Ser Val Thr Asn Val Gly Pro Arg Gly Gly Leu Ala Leu Ser Leu
 500 505 510
 Ser Pro Arg Leu Ala Pro Gly Ala Gly Ala Ser Ala Asn Gly His His
 515 520 525
 Gln Leu Pro Gly Tyr Val Lys His Gly Ser Ile Ser Glu Asn Ser Leu
 530 535 540
 Pro Ser Ser Gly Pro Glu Pro Gly Thr Lys Asp Asp Gly Tyr Leu Asn
 545 550 555 560
 Gly Ser Gly Leu Tyr Glu Pro Met Val Gly Glu Gln Pro Pro Pro Leu
 565 570 575
 Leu Glu Glu Glu Arg Glu Thr Val Met
 580 585

<210> 20
 <211> 591
 <212> PRT
 <213> Rattus rattus

<400> 20
 Met Gly Ala Ala Arg Ile Ala Pro Ser Leu Ala Leu Leu Leu Cys Cys
 1 5 10 15
 Pro Val Leu Ser Ser Ala Tyr Ala Leu Val Asp Ala Asp Asp Val Phe
 20 25 30
 Thr Lys Glu Glu Gln Ile Phe Leu Leu His Arg Ala Gln Ala Gln Cys
 35 40 45
 Asp Lys Leu Leu Lys Glu Val Leu His Thr Ala Ala Asn Ile Met Glu
 50 55 60
 Ser Asp Lys Gly Trp Thr Pro Ala Ser Thr Ser Gly Lys Pro Arg Lys
 65 70 75 80
 Glu Lys Ala Ser Gly Lys Phe Tyr Pro Glu Ser Lys Glu Asn Lys Asp
 85 90 95
 Val Pro Thr Gly Ser Arg Arg Arg Gly Arg Pro Cys Leu Pro Glu Trp
 100 105 110
 Asp Asn Ile Val Cys Trp Pro Leu Gly Ala Pro Gly Glu Val Val Ala
 115 120 125
 Val Pro Cys Pro Asp Tyr Ile Tyr Asp Phe Asn His Lys Gly His Ala
 130 135 140
 Tyr Arg Arg Cys Asp Arg Asn Gly Ser Trp Glu Val Val Pro Gly His
 145 150 155 160
 Asn Arg Thr Trp Ala Asn Tyr Ser Glu Cys Leu Lys Phe Met Thr Asn
 165 170 175
 Glu Thr Arg Glu Arg Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr
 180 185 190
 Val Gly Tyr Ser Met Ser Leu Ala Ser Leu Thr Val Ala Val Leu Ile
 195 200 205
 Leu Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met
 210 215 220
 His Met Phe Leu Ser Phe Met Leu Arg Ala Ala Ser Ile Phe Val Lys
 225 230 235 240
 Asp Ala Val Leu Tyr Ser Gly Phe Thr Leu Asp Glu Ala Glu Arg Leu
 245 250 255
 Thr Glu Glu Glu Leu His Ile Ile Ala Gln Val Pro Pro Pro Ala
 260 265 270
 Ala Ala Ala Val Gly Tyr Ala Gly Cys Arg Val Ala Val Thr Phe Phe
 275 280 285

Leu Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu
 290 295 300
 Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys Lys Tyr
 305 310 315 320
 Leu Trp Gly Phe Thr Ile Phe Gly Trp Gly Leu Pro Ala Val Phe Val
 325 330 335
 Ala Val Trp Val Gly Val Arg Ala Thr Leu Ala Asn Thr Gly Cys Trp
 340 345 350
 Asp Leu Ser Ser Gly His Lys Lys Trp Ile Ile Gln Val Pro Ile Leu
 355 360 365
 Ala Ser Val Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Ile Arg Val
 370 375 380
 Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr Arg
 385 390 395 400
 Gln Gln Tyr Arg Lys Leu Leu Arg Ser Thr Leu Val Leu Val Pro Leu
 405 410 415
 Phe Gly Val His Tyr Thr Val Phe Met Ala Leu Pro Tyr Thr Glu Val
 420 425 430
 Ser Gly Thr Leu Trp Gln Ile Gln Met His Tyr Glu Met Leu Phe Asn
 435 440 445
 Ser Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys Asn Gly
 450 455 460
 Glu Val Gln Ala Glu Ile Arg Lys Ser Trp Ser Arg Trp Thr Leu Ala
 465 470 475 480
 Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr
 485 490 495
 Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Ala
 500 505 510
 Gly Leu Ser Leu Pro Leu Ser Pro Arg Leu Pro Pro Ala Thr Thr Asn
 515 520 525
 Gly His Ser Gln Leu Pro Gly His Ala Lys Pro Gly Ala Pro Ala Thr
 530 535 540
 Glu Thr Glu Thr Leu Pro Val Thr Met Ala Val Pro Lys Asp Asp Gly
 545 550 555 560
 Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala Ser Gly Ser
 565 570 575
 Ala Arg Pro Pro Pro Leu Leu Gln Glu Gly Trp Glu Thr Val Met
 580 585 590

<210> 21

<211> 593

<212> PRT

<213> Homo sapiens

<400> 21

Met Gly Thr Ala Arg Ile Ala Pro Gly Leu Ala Leu Leu Leu Cys Cys
 1 5 10 15
 Pro Val Leu Ser Ser Ala Tyr Ala Leu Val Asp Ala Asp Asp Val Met
 20 25 30
 Thr Lys Glu Glu Gln Ile Phe Leu Leu His Arg Ala Gln Ala Gln Cys
 35 40 45
 Glu Lys Arg Leu Lys Glu Val Leu Gln Arg Pro Ala Ser Ile Met Glu
 50 55 60
 Ser Asp Lys Gly Trp Thr Ser Ala Ser Thr Ser Gly Lys Pro Arg Lys
 65 70 75 80
 Asp Lys Ala Ser Gly Lys Leu Tyr Pro Glu Ser Glu Glu Asp Lys Glu
 85 90 95
 Ala Pro Thr Gly Ser Arg Tyr Arg Gly Arg Pro Cys Leu Pro Glu Trp
 100 105 110
 Asp His Ile Leu Cys Trp Pro Leu Gly Ala Pro Gly Glu Val Val Ala
 115 120 125

Val Pro Cys Pro Asp Tyr Ile Tyr Asp Phe Asn His Lys Gly His Ala
 130 135 140
 Tyr Arg Arg Cys Asp Arg Asn Gly Ser Trp Glu Leu Val Pro Gly His
 145 150 155 160
 Asn Arg Thr Trp Ala Asn Tyr Ser Glu Cys Val Lys Phe Leu Thr Asn
 165 170 175
 Glu Thr Arg Glu Arg Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr
 180 185 190
 Val Gly Tyr Ser Val Ser Leu Ala Ser Leu Thr Val Ala Val Leu Ile
 195 200 205
 Leu Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met
 210 215 220
 His Leu Phe Leu Ser Phe Met Leu Arg Ala Val Ser Ile Phe Val Lys
 225 230 235 240
 Asp Ala Val Leu Tyr Ser Gly Ala Thr Leu Asp Glu Ala Glu Arg Leu
 245 250 255
 Thr Glu Glu Glu Leu Arg Ala Ile Ala Gln Ala Pro Pro Pro Pro Ala
 260 265 270
 Thr Ala Ala Ala Gly Tyr Ala Gly Cys Arg Val Ala Val Thr Phe Phe
 275 280 285
 Leu Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu
 290 295 300
 Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys Lys Tyr
 305 310 315 320
 Leu Trp Gly Phe Thr Val Phe Gly Trp Gly Leu Pro Ala Val Phe Val
 325 330 335
 Ala Val Trp Val Ser Val Arg Ala Thr Leu Ala Asn Thr Gly Cys Trp
 340 345 350
 Asp Leu Ser Ser Gly Asn Lys Lys Trp Ile Ile Gln Val Pro Ile Leu
 355 360 365
 Ala Ser Ile Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Val Arg Val
 370 375 380
 Leu Ala Thr Lys Gln Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr Arg
 385 390 395 400
 Gln Gln Tyr Arg Lys Leu Leu Lys Ser Thr Leu Val Leu Met Pro Leu
 405 410 415
 Phe Gly Val His Tyr Ile Val Phe Met Ala Thr Pro Tyr Thr Glu Val
 420 425 430
 Ser Gly Thr Leu Trp Gln Val Gln Met His Tyr Glu Met Leu Phe Asn
 435 440 445
 Ser Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys Asn Gly
 450 455 460
 Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala
 465 470 475 480
 Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr
 485 490 495
 Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val
 500 505 510
 Gly Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr Thr
 515 520 525
 Asn Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro Ala
 530 535 540
 Leu Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro Lys Asp
 545 550 555 560
 Asp Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala Ser
 565 570 575
 Gly Pro Glu Arg Pro Pro Ala Leu Leu Gln Glu Glu Trp Glu Thr Val
 580 585 590
 Met